



SEQUENCE LISTING

<110> Petzelt, Christian
<120> Cytotoxic Cyplasin of the Sea Hare, Aplysia Punctata, cDNA
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<140> 10/501,098
<141> 2004-12-06
<150> PCT/EP02/14511
<151> 2002-12-18
<160> 5
<170> PatentIn version 3.3
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Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
35 40 45
Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
50 55 60
Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
65 70 75 80
Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
85 90 95
Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
100 105 110
Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
115 120 125
Arg Tyr Tyr Leu Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr
130 135 140
Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
145 150 155 160

Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
 165 170 175

Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp
 180 185 190

Gly Arg Leu Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
 195 200 205

Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
 210 215 220

Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His
 225 230 235 240

Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
 245 250 255

Met Gln Lys Val Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser
 260 265 270

Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
 275 280 285

Ser Lys Ser Asp Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr
 290 295 300

Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
 305 310 315 320

Cys Thr Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
 325 330 335

Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
 340 345 350

Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
 355 360 365

Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
 370 375 380

Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu
 385 390 395 400

Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn
 405 410 415

Thr Leu Phe Gln Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly
 420 425 430

Ser Glu Ala Gly Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile
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Leu Asp His Leu Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln
 450 455 460

Glu Pro Lys Thr Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly
 465 470 475 480

Cys Gly Trp Ile Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met
 485 490 495

Asn Thr Met Arg Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly
 500 505 510

Ala Asp Tyr Ser Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu
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Glu Thr Ser Tyr Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser
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His Asn Val Gln Pro Pro Ser His Met Ala Ser His Val Gly
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<213> Aplysia punctata

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Gln Cys Asp Lys Thr Leu Asp Val Ala Ile Val Gly Ala Gly Ala Ala
 35 40 45

Gly Ala Tyr Ser Ala Tyr Leu Leu Arg Asn Lys Gly Gln Asn Ile Gly
 50 55 60

Val Phe Glu Phe Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln
 65 70 75 80

Leu Pro Asn Thr Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr
 85 90 95

Ile Thr Gly Ala His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly
 100 105 110

Leu Thr Pro Val Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr
 115 120 125

Arg Tyr Tyr Pro Arg Gly Gln Ser Leu Thr Phe Gln Glu Ala Leu Thr
 130 135 140

Gly Asp Val Pro Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp
 145 150 155 160

Asn Ile Phe Ala Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly
 165 170 175

Asp Gly Phe Val Thr Arg Glu Gln Leu Leu Lys Leu Arg Ala Ser Asp
 180 185 190

Gly Arg Pro Leu Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val
 195 200 205

Ala Ser Pro Glu Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr
 210 215 220

Thr Glu Val Ser Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His
 225 230 235 240

Leu Gly Glu Asp Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly
 245 250 255

Met Gln Lys Val Pro Glu Gln Pro Leu Arg Ala Phe Gly Asn Ser Ser
 260 265 270

Val Phe Gly His Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg
 275 280 285

Ala Lys Ser Asp Lys Ser His Val Pro Tyr Phe Arg Pro Thr Ser Thr
 290 295 300

Val Asp Gly Lys Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val
 305 310 315 320

Cys Ala Arg Gln Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln
 325 330 335

Val Asp Trp Pro Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly
 340 345 350

Ala Val Arg Thr Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln
 355 360 365

Pro Trp Trp Leu Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr
 370 375 380

Lys Gly Asp Thr Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Pro Asn
 385 390 395 400

Val Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Ser Thr
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Gln Pro Trp Ile His
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 <213> Artificial Sequence

<220>
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Cys Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn Thr
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Pro Asp Val Gln Leu Glu Leu Gly Gly Met Arg Tyr Ile Thr Gly Ala
 35 40 45

His Asn Leu Leu Glu Gly Val Val Arg Gln Leu Gly Leu Thr Pro Val
 50 55 60

Val Phe Thr Glu Gly Phe Gly Lys Leu Gly Arg Thr Arg Tyr Tyr Leu
 65 70 75 80

Arg Gly Gln Ser Leu Thr Phe Gln Glu Val Leu Thr Gly Asp Val Pro
 85 90 95

Tyr Asn Leu Thr Val Ala Glu Lys Gln Asn Gln Asp Asn Ile Phe Ala
 100 105 110

Phe Tyr Leu Lys Glu Leu Thr Arg Phe Asp Val Gly Asp Gly Phe Val
 115 120 125

Thr Arg Glu Gln Leu Leu Lys Leu Arg Val Ser Asp Gly Arg Leu Leu
130 135 140

Tyr Gln Leu Thr Phe Asp Glu Ala Leu Asp Leu Val Ala Ser Pro Glu
145 150 155 160

Gly Lys Glu Phe Ala Arg Asp Ile His Val Phe Thr Thr Glu Val Ser
165 170 175

Asp Asp Ala Asn Ala Val Ser Val Phe Asp Asp His Leu Gly Glu Asp
180 185 190

Gly Val Gly Glu Glu Ile His Thr Val Gln Glu Gly Met Gln Lys Val
195 200 205

Pro Glu Gln Leu Leu Arg Ala Phe Gly Asn Ser Ser Val Phe Gly His
210 215 220

Arg Val Phe Thr Asn Leu Gln Leu Lys Ala Ile Arg Ser Lys Ser Asp
225 230 235 240

Lys Ser His Val Leu Tyr Phe Arg Thr Thr Ser Thr Val Asp Gly Lys
245 250 255

Thr Thr Ile Leu Lys Phe Glu Pro Leu Gln Lys Val Cys Thr Arg Gln
260 265 270

Ile Ile Leu Ala Leu Pro Val Phe Ala Leu Met Gln Val Asp Trp Pro
275 280 285

Pro Leu Arg Glu Asn Arg Ala Gln Lys Ala Tyr Gly Ala Val Arg Thr
290 295 300

Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
305 310 315 320

Gln Asn Asp Val Thr Asp Phe Pro Ala Phe Val Thr Lys Gly Asp Thr
325 330 335

Thr Phe Ser Gln Met Tyr Asp Trp Lys Lys Ser Glu Ala Ser Gly Asp
340 345 350

Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly Asn Asn Thr Leu Phe Gln
355 360 365

Arg Val Leu Arg Asp Gln Gly Glu Pro Ile Asn Gly Ser Glu Ala Gly
370 375 380

Ala His Ile Val Ser Glu Pro Leu Lys Asn Gln Ile Leu Asp His Leu
385 390 395 400

Ala Asp Ala Phe Gly Val Pro Arg Ser Asp Ile Gln Glu Pro Lys Thr
405 410 415

Ala Val Ser Lys Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile
420 425 430

Thr Trp Arg Ala Gly Tyr His Phe Asp Asp Val Met Asn Thr Met Arg
435 440 445

Arg Pro Ser Leu Thr Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser
450 455 460

Trp Gly Leu Ile Ser Ser Trp Val Glu Gly Ala Leu Glu Thr Ser Tyr
465 470 475 480

Glu Val Ile Asp Thr Tyr Phe Lys Ser Glu Arg Ser His Asn Val Gln
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Pro Pro Ser His Met Ala Ser His Val Gly
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ctgaccccg tagtgtttac agaaggcttc ggtaagctgg gccgtacacg ctattacctg 240
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atggcctccc acgtgggc 1518

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